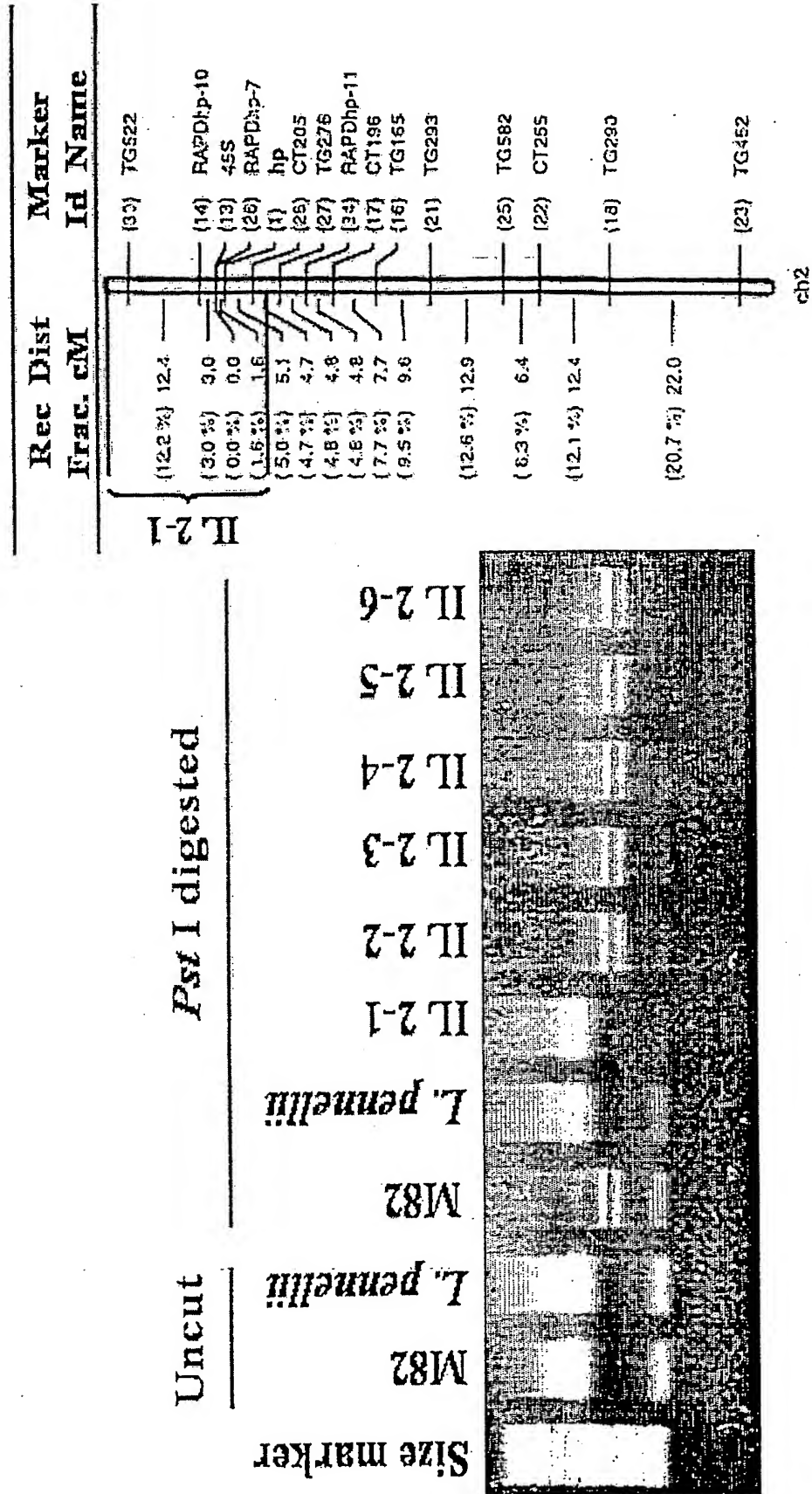


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Fig. 1.

CTCATGAGAAGGAGAAGTGCCTCAGCATTCTCTAGACTGTCATTTCTACTTTAGCTGAGT  
TGCTGGGAATGAAATCTTCTCTTGTACCCCTGCCTGGTTGCTGGAATAAAAATGTTTAAT  
TTGGATTGTTAACCTGTTTTCCAGAGTTACCGGACTCAAAATTGAGCTACTGGGGGAAAC  
TTCTATTGCATCAACCATATCATACCTAGACA/TATGCTTTTGTCTTCATTGGCTCAAG  
CTACGGAGATTACAGGTACTTTTAACTGTTGAGTGCATCTTGGTGCAATAAGTTGGTTT  
TTAGAGCTGCCTTATTGTATTTTCCATACAGTAGCCTTTCATTTCATTGGAACATTGAGG  
TTTTAAATTTAGTTGCCTATTTCTGGTGGTGCTTCATATTTACAGTTCCACTAATATT  
TTTGAATTCAGTTTAGCTTGTAAGCTCAATCTCCAGCCTGACACCAA

Fig. 2



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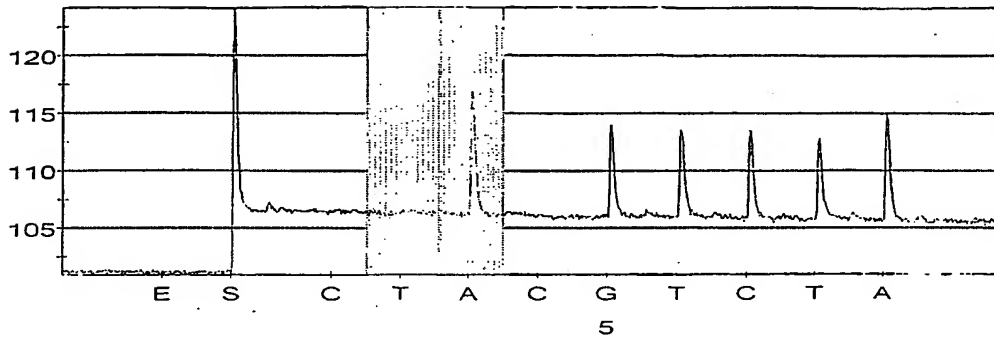
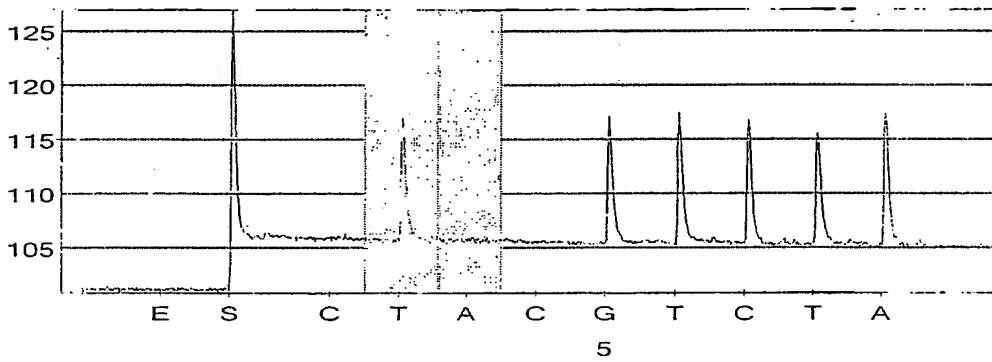
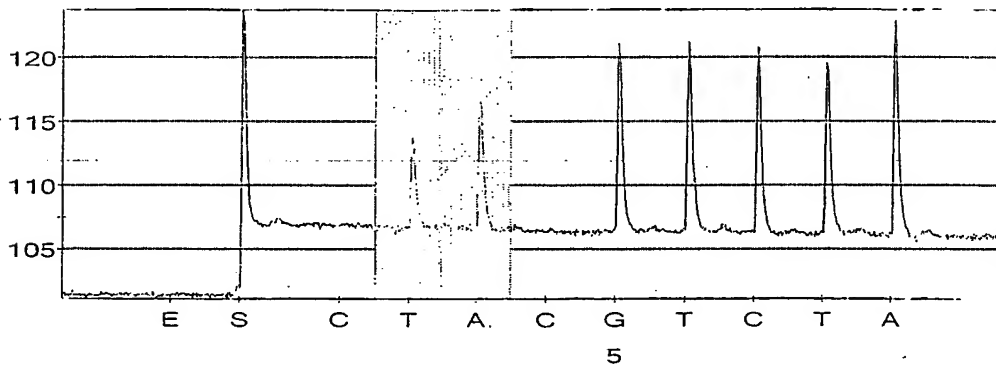
**Fig. 3**a. *hp-1/hp-1*b. *+/+*c. *hp-1/+*

Fig. 4

a. hp-1 (Asn>Tyr)

Gg 285 LEKEEQMDGTVTLKDDRVVLLGGETSIAECLTYLDNGVVFVGSRLGDSQLVKLNVD SNEQG  
 Hs 285 LEKEEQMDGTVTLKDDRVVLLGGETSIAECLTYLDNGVVFVGSRLGDSQLVKLNVD SNEQG  
 Dm 285 LGTAETSKG-VTVKDKVEQLGGEISIPCECTTYLDNGFLYICARHGDSQLVRLNSEAID-G  
 At\_DDB1B 282 ITHEK-----EKVTGLKIELLGETSIASSISYLDNAVVFVGSY GDSQLKLNLPDANG  
 At\_DDB1A 282 ITHEK-----EKVTGLKIELLGETSIASTISYLDNAVVFVGSY GDSQLVKLNLPDANG  
 Le 282 ITHEK-----EKVTGLKIELLGETSIASTISYLDNAVVFVGSY GDSQLVKLNLPDANG  
 Os 283 LTHERR-----ERVTKLIEYLGETSIASSISYLDNGVVVGSRF GDSQLVKLNLPDANG  
 Sp 293 ALFTD-----ETVSMELKELGESIASCLIALPDNHLFVGSFNNSVLLQLPSITKNN-

b. hp-1<sup>w</sup> (Glu>Lys)

Gg 817 VSKLKGKDPNTYFIVGTAMVYPPEEAEPKQGRIVVFHYS-DGKLQSLAEKEVKGAVYSMVE  
 Hs 817 VSKLKGKDPNTYFIVGTAMVYPPEEAEPKQGRIVVFQYS-DGKLQTVAEKEVKGAVYSMVE  
 Dm 818 MSAKLGDDPNNTYVAVATSLVIPLEEPEPKVGRILTFHYH-ENKLTQVAETKVDGTCVALVE  
 At\_DDB1B 772 LSCSFTDDKNVYCVGTAYVLPPEENETPKGRILVIVE-EGRLQLITTEKETKGAVYSINA  
 At\_DDB1A 772 LSCSFTEDKNVYCVGTAYVLPPEENETPKGRILVIVE-DGRLLQIAEKEVKGAVYSINA  
 Le 773 LSCSFSDDSNVYCHGTAYVMPPEENETPKGRILVIVE-DGKLQIAEKEVKGAVYSINA  
 Os 774 LSCSFSDDNNVYCVGTAYVLPPEENETPKGRILVAVE-DGRLLQIVTEKETKGAVYSINA  
 Sp 762 ILMNDDKR-----VVVGTGFNFEPDQDAPDSGRILMVFEMTSDNNTMQAEHKVQGSVNTLVL

Fig. 5

1 ATGAGTGATGGAACACTACGTGGTTACGGCTCACAAACCAAAATGTTACACATTCTCTGTGTGGCAATTTACCCGGTCC  
81 TCAAGAGCTCAATCTTATCATTTGGAAATGACTCGAATCGAGATTCAATTTACTCTCCCAAGGTTACAGCCTATGT  
161 TAGATGTGCCAATATATGGGAGATCGCGACACTTGAGCTTTTTCGTCCTCACGGTGAACACACAGATCTTCTCTTCATC  
241 GCAACAGAGCGATATAAATTTCTGTGCTTCAATGGGATACCTGAGGCATCTGAAGTTATCACAGAGCAATGGGAGATGT  
321 GTCAGACCGAATAGGCCGTCCACACAGATAATGGTCAGATTGGTATAATGATCCAGATTGCAGATTGATCGGGCTACATC  
401 TTTATGATGGACTATTTAAGGTTATTCCATTGTGATAACAAAGGCCAACTGAAGGAAGCTTTTAAACATCAGGCTCGAGGAG  
481 CTTCAAGTTTTAGATATTAAATTTCTGTATGTTGCCCAAGCCACAAATGTTGTTCTATATCAGGATAACAAAGGATGC  
561 CCGGCATGTCAAAACATATGAGGTGTCCTTGAAGAACAAGATTTTTATGAAGGCCCATGGGCTCAAAATAATCTTGATA  
641 ATGGAGCTTCTTTGCTAATACCACTACCTCCACCACCTGTGTGGTGTATTGATTATTGGAGAAGAAACCATCGTTTATTGC  
721 AGCGCTTCAGCTTTTAAGGCTATCCCAATTAGACCTTCTATCACAAAGAGCATATGGCGGGTTGATGCTGATGGTTCTCG  
801 ATATTGCTTGGGATCATAAATGGGCTTCTTCACTACTTGTAACTCATGAGAAGGAGAAAGTTACCGGACTCAAAA  
881 TTGAGCTACTGGGGAAACTTCTATTGCATCAACCATATCATACCTAGACAATGCTTTTGTCTTCTTCTTGGCTCAAGCTAC  
961 GGAGATTACAGCTTGTAAGCTCAATCTCCAGCCTGACACCAAGGTTCTTATGTGGAAGTTCTAGAGAGATATGTCAA  
1041 TTTAGGACCTATTGTGGACTTCTGTGTTGATCTGGAAGGCAAGGTCAGGTCAGGTTGTAACCTTGTCTGAGGCTT  
1121 ATAAAGGATGGATCACTTCGTATGTTTCGAAATGGAATGGCATAAATGAACAGGCGTCTGTGGAACCTACAAGGATCAAA  
1201 GGAATGTGGTCTTTAGATCTGCTACTGATGATCCATATGACACATTCTTGTGTTGTAGCTTCATTAGTGAACACACGCGT  
1281 TTTGGCTATGAACCTTGAGGATGAGCTGGAAGAACTGAGATAGAAGGCTTCAATCTCAAGTCCAGACCTTGTTTGTGTC  
1361 ATGATGCTGTATACAAACAGCTTGTTCAGGTTACTTCAAAATCTGTTAGATTGGTCAGTTCTACCTCTAGAGATCTGAAA  
1441 AACGAGTGGTTTGGCCCCAGTCGGCTACTCGGTCAATGTTGCAACTGCTAATGCCACTCAGGTACTATTGGCTACTGGGGG  
1521 TGGCCATCTGGTATACCTAGAAAATGGTGATGGGGTGTGAATGAAGTAAATAATGCCAAGTTGGATTATGATATCTCGT  
1601 GCCTGGACATAAATCCAAATGGTGAAAATCCGAACACTACAGTAACATTGCAGCAGTTGGAATGTGGACAGACATAAGTGTC  
1681 AGGATATATTCACTTCCTGACTTGAATCTCATTTACAAAGGAACAGCTAGGAGGGGAGATAAATTCCTCGTTCTGTTCTGAT  
1761 GTGTTCTTCCGAAAGGAVATCTTATCTACTATGTGCTTTGGGAGATGGCCATCTCTTGAATTTTGTATTGAGCATGAGTA  
1841 CTGGTGAAGCTGACAGATAGGAAAAAAGTTTCTCTTGGACACAGCCCCATAACACITTCGTACATTCTCATCTAAAGATACT

1921 ACACATGTCTTTGCTGCCTCCGATAGGCCAACACAGTTATTACAGCAGTAACAAGAAGCTGCTTTATAGCAATGTAATCT  
2001 AAAAGAGTTAGTCATATGTGCCCCATTCAATGTTGCAGCTTTTCCAGACAGCCTTGCAATCGCTAAAGAAGGTGAGTTAA  
2081 CAATTGGCACTATTGATGAATTCAAAAGCTTCACATTCTGTTCAATACCCCTTGGGAGCATGCACGTCCGATCAGCCAT  
2161 CAAGAGCAGACCCGGACATTTGCTCTATGCAGTGTGAAGTACTCAGTCAAAATGCAGATGATCCTGAAATGCATTTGT  
2241 CCGCCTGTTGGATGATCAGACATTTGAGTTCAATCAACATATCCCTTGACCAATTTGAATATGGCTGTTCCATACTAA  
2321 GCTGCTCCTTTTCTGATGATAGTAATGTGTATTATTGCAATTGGAACCTGCATATGTGATGCCAGAGGAAAATGAACCTACT  
2401 AAGGCCGGAATTTTAGTTTTTATAGTTGAAGATGGAAGCTCCAGCTAATTGCTGAGAAGGAAACTAAGGGAGCTGTCTA  
2481 CTCCTAAATGCCCTTCAATGGGAAACTGCTTGCTGCAATCAATCAGAAGATTCAATTGTACAAGTGGCTTCGCGTGAGG  
2561 ATGGTGGCAGCCGAGAAATTGCACACAGAAATGTGGACACCATGGTCATATATTAGCTCTTTATGTTCAAAACACGTGGGGAT  
2641 TTCATTGTTGTTGGTGATTTGATGAAATCCATTCTCTGCTGATTTTCAAGCATGAAGAGGTGCTATAGAGGAGCGAGC  
2721 CAGAGACTATAATGCAAAATTGGATGTGCTGATGATGACATTTATCTTGGTCTGAGAAATAACTTCA  
2801 ACCTTTTCACGGTCAGGAAAATAGTGAAGGTGCTACAGATGAGGAGCGCAGCCGCTTGAAGTGGTTGGTGAATACCAC  
2881 CTTGGCGAATTTGTTAATAGGTTAGACATGGTTCACTTCTCATGCGACTACCGACTACCAGATTCAGATGTTGGGCAGATACCCAC  
2961 TGTCATATTTGGCACAGTGAATGGTGTATTAGGGGTGATTGCATCACTACCTCATGATCAATATTTATTTTGGAGAAGC  
3041 TGCAGACAAACTTACGGAAAGTGATAAAGGGTGTGGGAGGTCTGAGCCATGAGCAGTGGAGGTGCTTTTACATGAGAAG  
3121 AAAACAGTAGATGCTAAAACCTTCTTGATGGAGATTTGATTGAATCATTCCTAGATCTTAGCAGGAATAGGATGGAAGA  
3201 GATTTCAAAGGCTATGTTCAGTTCCTCAGTTGAGGAACCTAATGAAGAGAGTGGGAAGAGTTGACAAGGTTGCATTAG

Fig. 6

1 MSVWNYVTAHKPTNVTHSCVGNFTGPQELNLIIAKCTRIEIHLLTPQGLQPMLDVPIYGRIATLELFRPHGETQDLLFI  
81 ATERYKFCVLQWDTEASEVITRAMGDVSDRIGRPTDNGQIGIIDPCRLIGHLYDGLFKVIPFDNKGQLKEAFNIRLEE  
161 LQVLDIKFLYGCCKPTIVVLYQDNKDARHVKTIEVSLKDKDFIEGPAQNNLDNGASLLIPVPPPLCGVLIIGEETIVYC  
241 SASAFKAIPRPSITRAYGRVDADGSRYL LGDHNGLLHLLVITHEKEKVTGLKIELLGSETSIASTISYLDNafvfigssy  
321 GDSQLVKNLQPDTKGSYVEVLERYVNLGPIVDFCVVDLERQGGQVVTCSGAYKDGSLRIVRNGIGINEQASVELQGIK  
401 GMWSLRSATDDPYDTFLVVSFISETRVLAMNLEDELEETEIEGFNSQVQTLFCHDAVYNQLVQVTSNSVRLVSSTSRDLK  
481 NEWFAPVGYSVNVATANATQVLLATGGGHLVYLEIGDGVNLNEVKYAKLDYDISCLDINPIGENPNVSNIAAVGMWTDISV  
561 RIYSLPDLNLITKEQLGGEIIPRSVLMCSFEGISYLLCALGDGHLNLFVLSMSTGELTDRKKVSLGTPITLRTFSSKOT  
641 THVFAASDRPTVIYSSNKKLLYSNVNLKEVSHMCPFNVAAPDLSLAIKEGELTIGTIDEIQKLHRSIPLGEHARRISH  
721 QEQTRTFALCSVKYTQSNADDPMEHFVRLDDQTFEFISTYPLDQFEYGCSSILSCSFSDDSNVYICIGTAYVMPEENEPT  
801 KGRILVFIVEDGKLQIAEKETKGAVYSNLAFNGKLLAAINQIOLYKWAASREDGGSRELQTECGHHGHILALYVQTRGD  
881 FIWGDLMKSISLLIFKHEEGAIEERARDYNANWMSAVEILDDDIYLGAEENNENFTVRKNSEGADEERSRLLEVVEYH  
961 LGEFVNRFRHGSLVMRLPDSVDVGQIPTVIFGTVNGVIGVIAASLPHDQYLFLEKQLTNLRKVIKGVGGLSHEQWRSFYNEK  
1041 KTVDAKNFLDGD LIESFLDLSRNRMEEISKAMSVPVEELMKRVEELTRLH